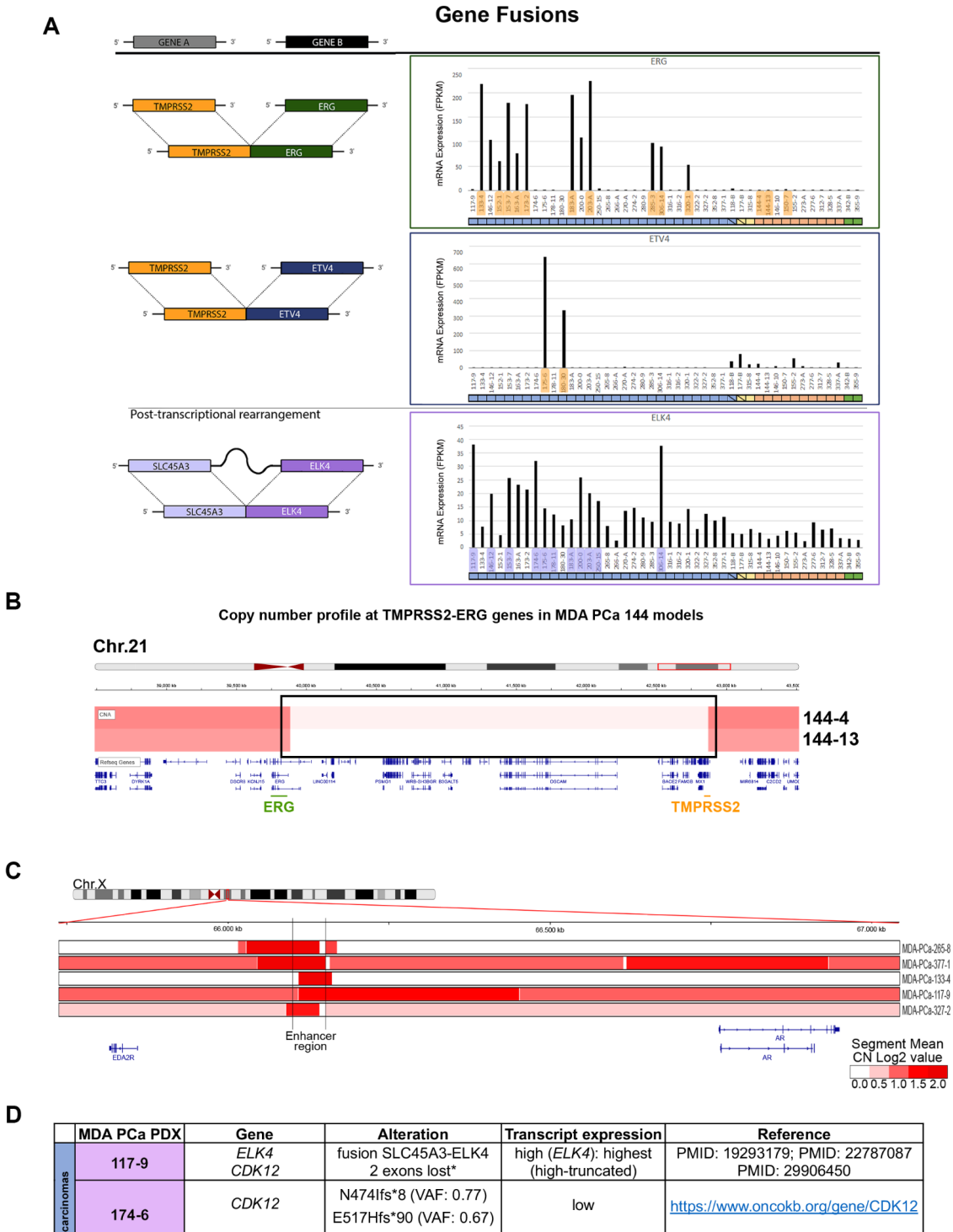
Figure S3



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	MDA PCa PDX	Gene	Alteration	Transcript expression	Reference
Adenocarcinomas	117-9	*ELK4* *CDK12*	fusion SLC45A3-ELK4 2 exons lost*	high (*ELK4*): highest (high-truncated)	PMID: 19293179; PMID: 22787087 PMID: 29906450
	174-6	*CDK12* *ELK4*	N474Ifs*8 (VAF: 0.77) E517Hfs*90 (VAF: 0.67) fusion SLC45A3-ELK4	low high (*ELK4*)	https://www.oncokb.org/gene/CDK12
	175-6	*ETV4*	fusion TMPRSS2-ETV4	high (*ETV4*)	PMID: 16585160; PMID: 30033370
	280-9	*AXIN1*	G1549A (VAF: 0.98)	low	PMID: 18514389

*detected on RNAseq profile

Fig S3. Fusion genes expression levels. CNV details on TMPRSS2-ERG fusion and AR enhancer region. Putative PCa drivers in models lacking alterations in four major genes. A. Representation of fusions identified (left) associated with high RNA expression levels of gene B (right) in the MDA PCa PDX cohort studied. Models in which fusions were detected are highlighted in orange for TMPRSS2 and in light violet for SLC45A3. TMPRSS2: transmembrane serine protease 2; ERG: ETS-related gene; ETV4: ETS variant transcription factor 4; ELK4: ETS transcription factor ELK4; SLC45A3: solute carrier family 45 member 3; FPKM: fragments per kilobase of transcript per million mapped reads. **B.** Detailed copy number profile in Chromosome 21 for MDA PCa 144-4 and 144-13 models derived from two areas of the same tumor, depicting region containing *TMPRSS2* and *ERG* genes. **C.** Detail of segment Copy Number (CN) Log2 value in the region containing AR and its enhancer, for models with amplified enhancer region. **D.** Putative PCa drivers in models lacking alterations in four major genes. Note that only some of the oncogenic alterations found in these models are presented in the table.